National Aeronautics and Space Administration

American Society for Gravitational and Space Research (ASGSR) 2016

GeneLab Data Systems (GLDS) Workshop

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October 28th, 2016

Agenda

- GLDS Phase 1 Key Capabilities (Operational)
  - Background History
  - Current Phase 1 C-Gene Key System Capabilities
- GLDS Phase 2 Key Capabilities (Work-In-Progress)
  - Introduction
  - Phase 2 X-Gene Key System Capabilities
- GLDS Tutorial (Phase 1 C-Gene)
- Backup - GLDS Metrics
  - Usage Metrics (Downloads, Page Views, etc.)

GLDS Phase 1 Key Capabilities (Operational)

Background History

- GLDS Phase 1 (denoted as “C-Gene”) completed in April 2015 timeframe to implement and deploy as an **interim** solution as a data repository with simple search capability

- Initially imported 22 curated and V&V legacy data sets to Phase 1 C-Gene production system

- Phase 1 C-Gene is an operational system with routine maintenance for software enhancements (quarterly updates) & continuous data updates (6-8 weeks cycles)

- Publicly available at: https://genelab-data.ndc.nasa.gov/

Current Phase 1 C-Gene System (What's New) 1 of 2

- Since then, imported an additional 58 new & legacy curated, V&V data sets, including RR-1, ISS Microbial Observatory, zebrafish, etc., to Phase 1 C-Gene production system:
  - As of Release 1.0.14 deployed on 9/22/16, there is a total of **80 data sets** available for the general public

- Improved data importing script and optimize process to reduce site maintenance time (e.g., do not need to bring down production site during data updates)

Current Phase 1 C-Gene System (What's New) 2 of 2

- C-Gene Phase 1 C-Gene Operational System:
  - Software Enhancements:
    - Enhanced pagination (e.g., drop-down list of number of data sets displayed per page: defaults to 25 per page)
    - Added links to useful bioinformatics data mining & visualization tools (e.g., cBioPortal, Cistrome, GenePattern, GenomeSpace, ISA Tools, etc.)
    - Implemented a link to JSC Life Sciences Data Archive (LSDA) data request access portal based on certain metadata fields and values
    - Added GLDS accession numbers on the listing/browsing of data sets
    - Added a link to download the most recent GeneLab customized ISACreator configuration zip package for general public usage
    - Provided updates to genelab.nasa.gov contents (e.g., recent announcements, events, etc.)
    - Provided fixes to improve Look&Feel User Interfaces/Experience (UI/UX) (e.g., Mobile vs. Desktop screen sizes, intuitiveness)

Phase 1 C-Gene Key Capabilities

- Leverage from existing NASA C3 core software platform and infrastructure (e.g., Don't reinvent the wheel!)
  - C3 successfully used by other NASA Programs/Projects (e.g., DASHlink, NASA Earth Exchange (NEX), and Applied Sciences Program Water Resources)
- Primary used as a data repository and displaying relevant metadata fields
- Browse and navigate user interfaces
- Download curated and V&V data sets as compressed zipped files
- Simple keyword search using regular expressions (e.g., pattern matching on certain fields like Title, unique GLDS Accession Numbers Study Description, Organisms, Contact Names, etc.)
- Links to relevant publications (if available)

Current Phase 1 C-Gene Site (1 of 3)

GeneLab
Open Science for Exploration

http://genelab.nasa.gov

Current Phase 1 C-Gene Site (2 of 3)

https://genelab-data.ndc.nasa.gov/genelab/

GeneLab
Open Science
for Exploration

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NASA GeneLab Data Repository

NASA GeneLab will expand scientists' access to experiments that explore the molecular response of terrestrial biology to spaceflight environments. The vast amounts of raw data generated by experiments aboard the International Space Station will be made available to a worldwide community of scientists and computational researchers.

This data repository holds NASA's space biology datasets.

For more information about NASA GeneLab, please refer to our overview website at genelab.nasa.gov. Another source of information is the GeneLab Strategic Plan.

Study Metadata

Study data hosted in the repository include a metadata definition file that is formatted according the ISA-Tab specification, which is viewable using the ISA Tools ISACreator program using a customized GeneLab configuration. Consumers of the metadata files should load this configuration, ISA configuration files, into the ISACreator program prior to loading the ISA-Tab file set, in order to view the study metadata completely and correctly.

GeneLab Sponsors

NASA GeneLab is sponsored by the NASA Space Life and Physical Sciences Research and Applications Division (SLPSRA) and the NASA International Space Station Program.

Contributing Datasets to GeneLab

Please refer to our data submission process to contribute your data to NASA GeneLab.

Current Phase 1 C-Gene Site (3 of 3)

Metadata display

Simple Navigating and Browsing

GLDS-69

Microbial Observatory (ISS-MO): Indoor microbiome study of the International Space Station surfaces

Organisms	Factors	Assay Types	Release Date	Description
cellular organisms	spaceflight	metagenome profiling	07-Jul-2016	Presented here is the environmental microbiome study of the International Space Station surfaces. The environmental samples were collected with the polyester wipes from eight different locations in the ISS during two consecutive sampling se...

GLDS-68

Microbial Observatory (ISS-MO): Draft Genome Sequence of two Aspergillus fumigatus Strains Isolated from the International Space Station

Organisms	Factors	Assay Types	Release Date	Description
Aspergillus fumigatus	spaceflight	genome sequencing	08-Jul-2016	Aspergillus fumigatus is a saprophytic, filamentous fungus that is ubiquitous outdoors (soil, decaying vegetation) and indoors (hospitals, simulated closed habitats, etc.). A. fumigatus can adapt to various environmental conditions and form...

GLDS-67

Microbial Observatory (ISS-MO): Study of BSL-2 bacterial isolates from the International Space Station

Organisms	Factors	Assay Types	Release Date	Description
Enterobacter Staphylococcus aureus Pantoea conspicua Staphylococcus Klebsiella Acinetobacter pittii	spaceflight	genome sequencing	08-Jul-2016	In an on-going Microbial Observatory experimental investigation on the International Space Station (ISS), multiple bacterial isolates of Biosafety Level 2 (BSL-2) were isolated and identified. The antibiotic susceptibility pattern was teste...

GLDS-66

Microbial Observatory (ISS-MO): Antimicrobial resistance genes

Organisms	Factors	Assay Types	Release Date	Description
cellular organisms	spaceflight	environmental gene survey	07-JUL-2016	The environmental samples were collected with the polyester wipes from eight different locations in the International Space Station (ISS) during two consecutive sampling sessions (three months apart) within the ISS Microbial Observatory Exp...

Simple Metadata Display

Microbial Observatory (ISS-MO): Indoor microbiome study of the International Space Station surfaces

2 datasets available for download here:

Study Metadata Files

Metagenomic Sequencing Assay Data Files

GeneLab Accession Number	GLDS-69
Source Accession Number	N/A
Contacts	Name: Kasthuri Venkateswaran; Role: Principal Investigator; Organization: NASA; Email: kjvenkat@jpl.nasa.gov
Submission Date	03-May-2016
Public Release Date	07-Jul-2016
Study Description	Presented here is the environmental microbiome study of the International Space Station surfaces. The environmental samples were collected with the polyester wipes from eight different locations in the ISS during two consecutive sampling sessions (three months apart). The specific objective was to unveil the pool of genes for each location during two separate sessions to learn of functional and metabolic diversity of microorganisms in the ISS. The International Space Station (ISS) as a closed built environment has its own environmental microbiome which is shaped by microgravity, radiation, and limited human presence. The microbial diversity associated with ISS environmental surfaces was investigated during this study. Polyester wipes and contact slides were used for sampling of eight various surface locations on the ISS at different time periods. The samples were retrieved and analyzed immediately upon the return to the Earth (via Soyuz TMA-14M or Dragon capsule from SpaceX). After surface sample collection, contact slides containing nutrient media for the growth of bacteria and fungi were incubated at 25˚C. The polyester wipes were processed to measure microbial burden (R2A, Blood Agar, and Potato Dextrose Agar) and recover cultivable bacteria as well as fungi. Subsequently, viable microbial burden was assessed using Adenosine Triphosphate (ATP) assay, and quantitative polymerase chain reaction (PCR) methods after propidium monoazide (PMA) treatment. The 16S-tag and metagenome analyses were used to elucidate viable microbial diversity. The cultivable bacterial population yield from the polyester wipes was very high (5 to 7-logs) when compared with the contact slides (102 to 103 CFU/m2). The PMA-qPCR analysis showed considerable variation of viable bacterial population (105 to 109 16S rDNA gene copies/m2) among locations sampled. Unlike contact slides, polyester wipes cover much larger sample surface (~1 m2) and produce much more reliable results of the microbial diversity of the ISS covering both cultivable and non-cultivable species. The cultivable, total, and viable microbial diversity was determined utilizing state-of-the art molecular techniques. The implementation of the PMA assay before DNA extraction allowed distinguishing viable microorganisms, which is crucial for determining their role to the crew health, the ISS maintenance and the general knowledge of the closed environmentally controlled built systems.
Organisms	cellular organisms
Study Design Factor(s)	Factor: spaceflight; Ontology: Concept: Space Flight

GLDS Phase 2 Key Capabilities (Work-In-Progress)

GLDS Phase 2 X-Gene Introduction

- GLDS Phase 2 (denoted as "X-Gene") **Work-In-Progress**:
  - Focus on integrated full-text search & data federation key capabilities (e.g., data integration/fusion and mash-up)
  - Target Phase 2 completion (Release 2.0) with fully implemented capabilities available worldwide in Sept. 2017
  - Recently completed Release 1.1 (Phase 2 Iteration 1) on 9/14/16 as initial proof-of-concept integrated search + data federation with NIH/ NCBI's GEO database
  - Starting on Release 1.2 (Phase 2 Iteration 2) with target completion in Jan. 2017 with integrated search + data federation enhancements (e.g., add new external bioinformatics data sources)
  - Starting to solicit internal user feedback (e.g., looking for possible internal participants)

FY16 Realigned Trade Study

- A **Realigned** Trade Study:
  - The basis for new X-Gene system (Phase 2 and beyond)
  - Will eventually replace existing Phase 1 C-Gene operational system built on top of ARC-TI Center for Cross-discipline Collaboration (C3) platform
  - Takes lessons learned from FY15 trade study and will not start from scratch:
    - Select top 7 software platforms from FY15 with appropriate rationales + 3 new platforms not evaluated previously, such as:
      - NSF/University of Arizona's iPlant/CyVerse, Broad Institute's (Harvard/ MIT) GenomeSpace, and NASA's Athena platform
    - Total of 10 platforms to evaluate & assess for FY16

FY16 Trade Study Participants

- Reached out to 78 external participants from:
  - Science Council
  - Academia
  - Other Government Agencies (e.g., Veterans Affairs Dept., Lawrence Berkeley/Livermore National Labs, DoD, etc.)
  - NASA Space Biology, HRP, and other PIs
  - GeneLab Stakeholders (e.g., SLPS & ISSP)
  - Other NASA Centers (e.g., JSC, KSC, HQ, etc.)

- Received a total of 16 participants' Excel input submissions:
  - 7 external participants (e.g., representatives from VA Medical Center, U.S. Army Center for Environmental Health Research, Space Biology/HRP PIs, Science Council, Duke University, etc.) compared to last FY15 had 2 GL stakeholders as "external" participants
  - 9 internal GeneLab participants compared to FY15 had only 7 participants

FY16 Trade Study Analysis

- Statistical analysis on the following:
  - RAW Average (Mean) score across all 16 participants (0 through 5 ratings for each criteria) for each software platform (total of 10 platforms evaluated); Hence a total of 16 x 30 x 10 = 4,800 data points.
  - Weighted Average (Mean) score across all participants for each platform with reassigned weight factor (e.g., all 30 criteria weight % must total 100%)
  - RAW Median score (e.g., what's the middle value)
  - RAW Mode score (e.g., most frequent occurred value)
  - Sampling vs. Population Variances (e.g., deviation from the mean)
  - Standard Deviations (e.g., measures the amount of variation)

- Other important factors & considerations:
  - Software Maintainability & Complexity
    - Count total physical Source Lines of Code (SLOC) to measure codebase size
    - Different popular programming languages used in bioinformatics field (e.g., Java, JavaScript, Python, Perl, R, etc.)
    - Number of files & comments in codebase
    - Number of source code repositories (e.g., GitHub and/or other locations)

FY16 Realigned Trade Study Results and Recommendation

	FY16 Trade Study (Ranked)	RAW Avg Score	Weighted Avg Score	RAW Median Score	RAW Mode Score	Sample Variance	Population Variance	Sample Std. Deviation	Population Std. Deviation
1	GenomeSpace	3.92	4.02	4.00	4.00	0.46	0.44	0.68	0.67
2	KBase	3.97	4.00	4.14	4.00	0.45	0.44	0.67	0.66
3	CyVerse	3.91	3.98	4.09	4.47	0.55	0.53	0.74	0.73
4	Arvados	3.67	3.78	3.76	3.62	0.41	0.40	0.64	0.63
5	Globus	3.58	3.64	3.79	4.00	0.46	0.44	0.68	0.64

- Top 5 highest ranked platform candidates by weighted average scores are:
  1. GenomeSpace from Broad Institute (Harvard/MIT)
  2. KBase from DOE's Office of Science
  3. CyVerse (formerly iPlant) from NSF & University of Arizona
  4. Arvados from Harvard University
  5. Globus from Computation Institute (University of Chicago & Argonne National Lab)

FY16 Realigned Trade Study Results and Recommendation

- Based on FY16 trade study results, the platform recommendation is…GenomeSpace!
  - Will meet programmatic maintainability of source codebase within resource guidelines
  - Predominately written in Java and JavaScript programming languages (current GLDS team has expertise!)
  - Provides modular system architecture & design for extensibility, scalability, flexibility, and performance using Service-Oriented Architecture (SOA), similar to GLDS generic reference system architecture
  - Best option for “T-Gene” and possibly “NRA Gene” capabilities
- Pivoting to new recommended software platform GenomSpace coming out of FY16 realigned trade study (e.g., migration plan for both software + data in Phase 2)

GLDS Phase 2 Strategic Bioinformatics Data Sources

- GeneLab identified 3 key strategic external bioinformatics data sources for Phase 2 integration:
  - NIH/NCBI's GEO database (Gene Expression Omnibus)
  - EBI's PRIDE database (Proteomics)
  - MG-RAST database (Metagenomics)

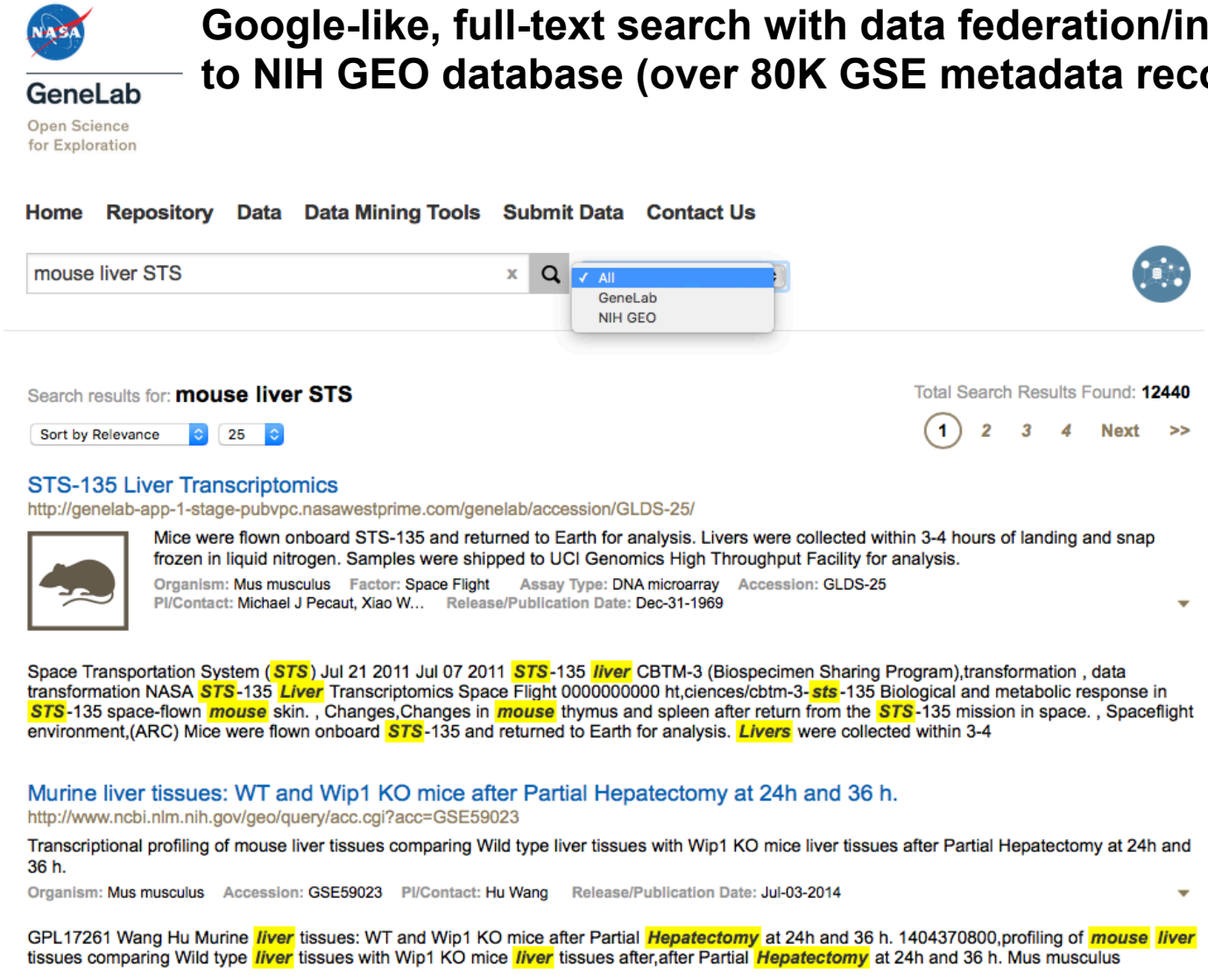
- Recommendations from GeneLab Steering Committee in July 2016 to possibly include:
  - Nuclear Receptor Signaling Atlas (NURSA)
  - NIH's Human Microbiome Project Data Analysis & Coordination Center (HMPDACC)
  - NIH/NCBI's database of Genotypes & Phenotypes (dbGaP)

GLDS Phase 2 X-Gene Key Capabilities

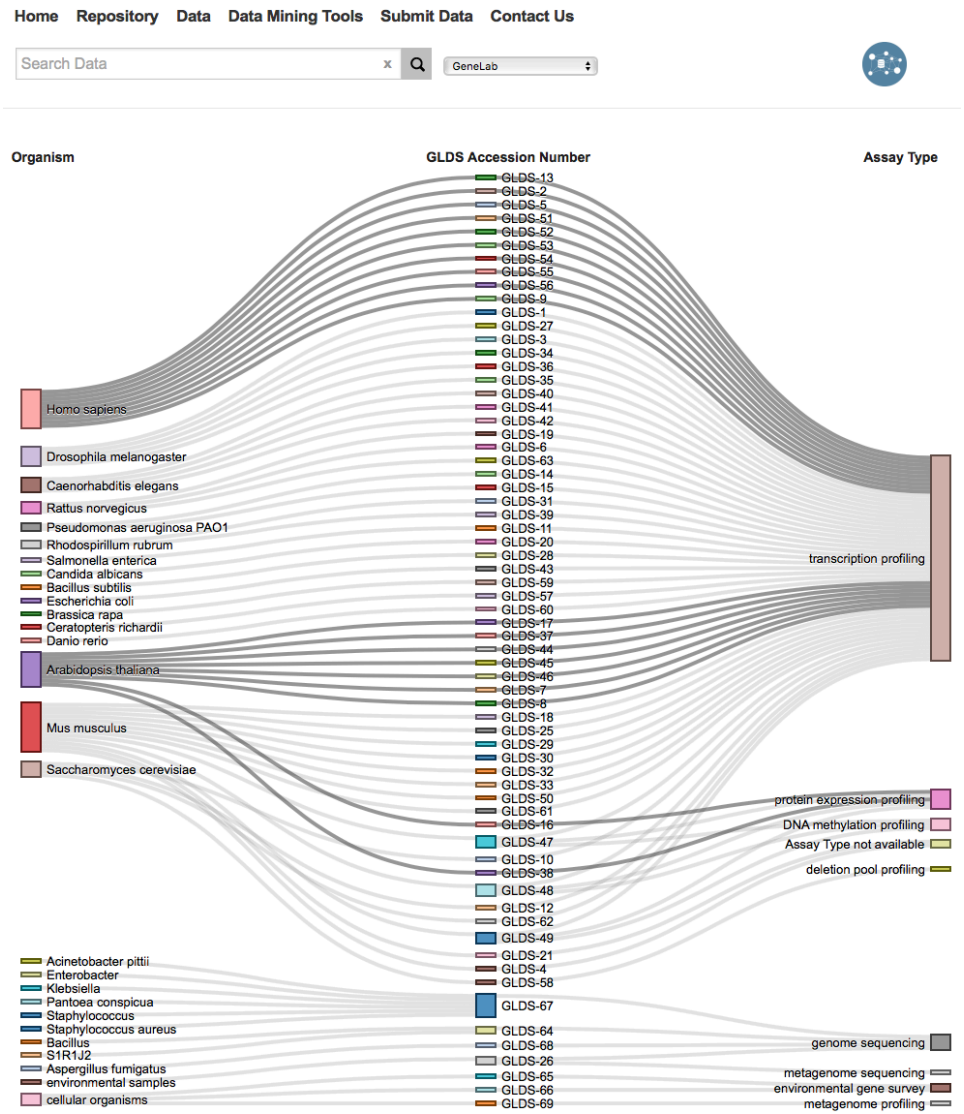
- GLDS Phase 2 X-Gene (Integrated Full-Text Search & Data Federation)
  - Release 1.1 deployed on 9/14/16
    - Prototype of integrated full-text search & data federation/ integration between GeneLab & NIH/NBCI's GEO databases (e.g., Google-like search engine)
    - Establish core Common Metadata Model (CMM) for easier data federation/integration to other bioinformatics databases
    - Customizable search ranking/relevancy algorithm
    - Provides Medical Subject Headings (MeSH) as a thesaurus for "smart" searching on metadata fields
    - Frequent GeneLab specific keyword search terms lookup
    - Data visualization (GLDS Organisms vs. Assay Types)
    - Automatic scripts to pull GEO data changes on nightly basis

Phase 2 X-Gene Release 1.1 Search and Federation

Google-like, full-text search with data federation/integration to NIH GEO database (over 80K GSE metadata records ingested)



Phase 2 X-Gene Release 1.1 Data Visualization



GLDS Tutorial (Phase 1 C-Gene)

Search Keywords Using GeneLab Phase 1 C-Gene

GeneLab
Open Science for Exploration

Enter keyword "liver" on search textbox

Home | Repository | Data | Data Mining Tools | Submit Data | Contact Us | liver

Page 1 of 4 (Total Studies: 80) Next >
Studies Per Page: 25

GLDS-83

Comparative Transcriptomic Analysis of Adult Medaka Tissues Sampled after Adaptation to a Space Environment

Organisms	Factors	Assay Types	Release Date	Description
Oryzias latipes	Spaceflight	transcription profiling	15-Oct-2015	To understand how humans adapt to space environments, many experiments can be conducted on astronauts while they work aboard the Space Shuttle or the International Space Station (ISS). We also need animal experiments that can apply to human...

GLDS-81

Bacillus subtilis strains at low-pressure: 5 kPa versus 101 kPa growth

Organisms	Factors	Assay Types	Release Date	Description
Bacillus subtilis	strain pressure	transcription profiling	14-Mar-2014	Comparing the transcriptional responses of Bacillus subtilis strains WN624 and WN1106 at 5 kPa and 101 kPa. WN1106 is a 5 kPa-evolved strain with increased fitness compared to ancestor-WN624 strain at 5 kPa. This experiment probed the diffe...

GLDS Search Results

5 search results for "liver"

Returned 5 search results for keyword “liver”

GLDS-63

Transcription profiling of rat response to changes in developmental stage - 3 types of tissue, 3 gravity conditions, 2 developmental conditions

Organisms	Factors	Assay Types	Release Date	Description
Rattus norvegicus	tissue microgravity developmental condition hypergravity	transcription profiling	27-Nov-2009	Transcriptional crosstalk between mammary gland, liver and adipose tissue Experiment Overall Design: Pregnant and Lactating rats exposed to 3 gravity conditions

GLDS-49

Multi-omic investigations of mouse liver subjected to simulated spaceflight freezing and storage protocols

Organisms	Factors	Assay Types	Release Date	Description
Mus musculus	freezing profile tissue storage time	DNA methylation profiling protein expression profiling transcription profiling	Feb-04-2016	This study compares standard laboratory protocols for tissue freezing and storage with a simulation of the delayed processing of liver specimens and long-term storage protocols used during the Rodent Research-1 (RR-1) payload. Liver samples...

GLDS-48

Rodent Research-1 (RR1) NASA Validation Flight: Mouse liver transcriptomic, proteomic, and epigenomic data

Organisms	Factors	Assay Types	Release Date	Description
Mus musculus	gravitation dissection condition	DNA methylation profiling transcription profiling protein expression profiling	Dec-15-2015	RR-1 is a validation flight to evaluate the hardware, operational and science capabilities of the Rodent Research Project on the ISS. RNA, DNA, and protein were purified from 14 livers from RR-1 mice (female, C57Bl6/J, 16wk old at time of l...

GLDS-47

Rodent Research-1 (RR1) National Lab Validation Flight: Mouse liver transcriptomic, proteomic, and epigenomic data

Organisms	Factors	Assay Types	Release Date	Description
Mus musculus	Gravitation Dissection Timeline	DNA methylation profiling protein expression profiling transcription profiling	15-Dec-2015	The Rodent Reasearch-1 National Lab (RR-1 CASIS) experiment was performed to study the effect of microgravity on muscle wasting. RNA, DNA, and protein were purified from nine RR-1 CASIS (the Center for the Advancement of Science in Space) l...

GLDS-25

STS-135 Liver Transcriptomics

Organisms	Factors	Assay Types	Release Date	Description
Mus musculus	Space Flight	transcription profiling	Oct 29 2015	Mice were flown onboard STS-135 and returned to Earth for analysis. Livers were collected within 3-4 hours of landing and snap frozen in liquid nitrogen.

GLDS Viewing & Navigating Study Data

GLDS-63

Transcription profiling of rat response to changes in developmental stage - 3 types of tissue, 3 gravity conditions, 2 developmental conditions

Organisms	Factors	Assay Types	Release Date	Description
Rattus norvegicus	tissue microgravity developmental condition hypergravity	transcription profiling	27-Nov-2009	Transcriptional crosstalk between mammary gland, liver and adipose tissue Experiment Overall Design: Pregnant and Lactating rats exposed to 3 gravity conditions

Click on title link for more information

GLDS-49

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STS-135 Liver Transcriptomics

GLDS Detailed Study Metadata

Rodent Research-1 (RR1) NASA Validation Flight: Mouse liver transcriptomic, proteomic, and epigenomic data

4 datasets available for download here:

Proteomics Data Files
Study Metadata Files
Bisulfite Sequencing Data Files
RNA-Seq Data Files

Option to download relevant data sets

GeneLab Accession Number	GLDS-48
Source Accession Number	
Contacts	

Name	Role	Organization	Email
Ruth Globus	RR1 Project Scientist	NASA ARC	ruth.k.globus@nasa.gov

Submission Date	
Public Release Date	Dec-15-2015
Study Description	RR-1 is a validation flight to evaluate the hardware, operational and science capabilities of the Rodent Research Project on the ISS. RNA, DNA, and protein were purified from 14 livers from RR-1 mice (female, C57Bl6/J, 16wk old at time of launch), including seven from the Flight group and seven from the Ground Control group. From each group, two liver samples were collected and frozen immediately after euthanasia (Flight mice dissected on-orbit after total 37 days after launch, Samples FLT-2,3 and corresponding Ground Control samples GC-21,22). An additional five samples from each group were collected from frozen carcasses dissected post-flight (Samples FLT-26,27,28,29,30 and corresponding Ground Control samples GC-36,37,38,39,40). RNA-Seq, whole genome BS-Seq (bisulfite sequencing) and proteomic expression profiling were performed.
Organisms	Mus musculus
Study Design Factor(s)	

Factor	Ontology: Concept
gravitation	Gravitation
dissection condition	dissection

Assay(s)

Assay Type	Device Type	Device Platform
DNA methylation profiling	nucleotide sequencing	Illumina
transcription profiling	nucleotide sequencing	Illumina
protein expression profiling	mass spectrometry	LTQ Orbitrap Velos (Thermo Scientific)

Project

Project Identifier	RR-1
Project Link	https://lsda.jsc.nasa.gov/scripts/experiment/exper.aspx?exp_index=13380
Project Type	Flight Study
Flight Program	International Space Station (ISS)
Experiment Platform	AEM-X Habitat
Space Program	NASA
Managing NASA Center	Ames Research Center (ARC)
Funding Source	This investigation was funded by the NASA Space Biology Program Office, Space Life and Physical Sciences Research and Applications Division, and additional funding from the

Select & Download Study Data

Datasets for Study: Rodent Research-1 (RR1) NASA Validation Flight: Mouse liver transcriptomic, proteomic, and epigenomic data

Total Data Volume: 367.2 GB

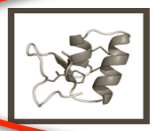
RNA-Seq Data Files

Raw sequencing files are in FASTQ format.

File Download Links:

GLDS-48_transcriptomics_N-GC-37.tar.gz (1.0 GB)
GLDS-48_transcriptomics_N-GC-36.tar.gz (1.1 GB)
GLDS-48_transcriptomics_N-GC-22.tar.gz (1.2 GB)
GLDS-48_transcriptomics_N-GC-21.tar.gz (1.1 GB)
GLDS-48_transcriptomics_N-FLT-3_.tar.gz (960.4 MB)
GLDS-48_transcriptomics_N-FLT-30.tar.gz (1.1 GB)
GLDS-48_transcriptomics_N-FLT-2_.tar.gz (1.3 GB)
GLDS-48_transcriptomics_N-FLT-28.tar.gz (1.1 GB)
GLDS-48_transcriptomics_N-FLT-26.tar.gz (1.2 GB)
GLDS-48_transcriptomics_N-FLT-27.tar.gz (1.1 GB)
GLDS-48_transcriptomics_N-FLT-25.tar.gz (1.1 GB)
GLDS-48_transcriptomics_N-GC-38.tar.gz (1.3 GB)
GLDS-48_transcriptomics_N-GC-39.tar.gz (1.0 GB)
GLDS-48_transcriptomics_N-GC-40.tar.gz (1.1 GB)
GLDS-48_transcriptomics_RR1-NASA.md5sum (2.8 KB)

Options to download either RNA-Seq or Proteomics data files



Proteomics Data Files

LC-MS3 Proteomics Data. Compressed collection of raw or processed data files and quality report associated with this study. Formats are platform specific. Please view the associated ISA-TAB metadata files to get formatting details.

File Download Links:

GLDS-48_proteomics_RR1-NASA.md5sum (1.5 KB)
GLDS-48_proteomics_RR1-NASA.raw.tar.gz (11.1 GB)
GLDS-48_proteomics_RR1-NASA.processed.tar.gz (8.4 GB)

Download Metadata Files and ISACreator Configuration

Study Metadata Files

ISA-Tab format file. Tab delimited Investigation, Study, and Assay level metadata. See ISA-tools.org for format details and software.

File Download Links:
GLDS-48_metadata_RR1-NASA-ISA.zip (9.0 KB)

Click link to download ISA-Tab formatted medata zip package

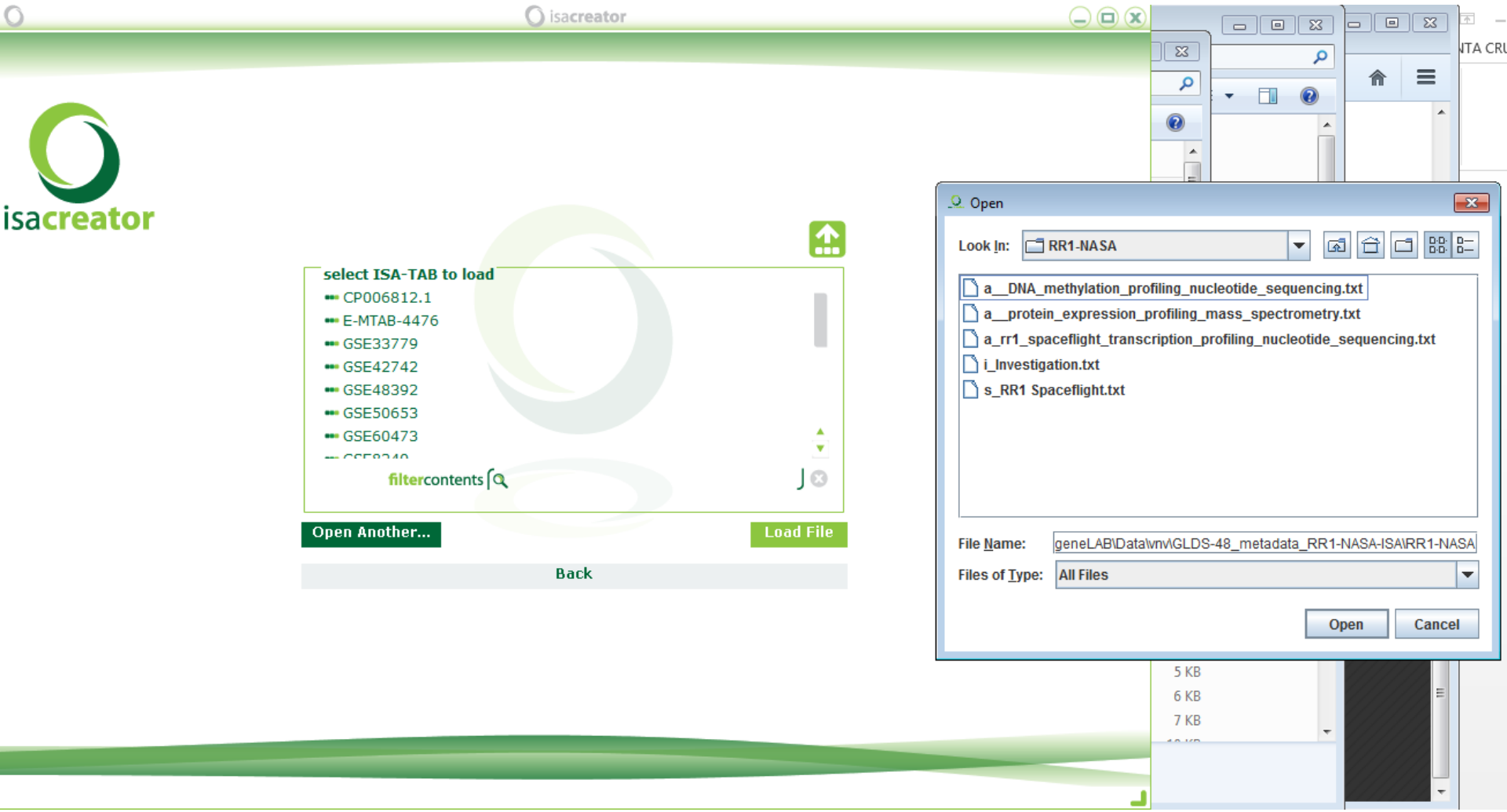
https://genelab-data.ndc.nasa.gov/

Study Metadata

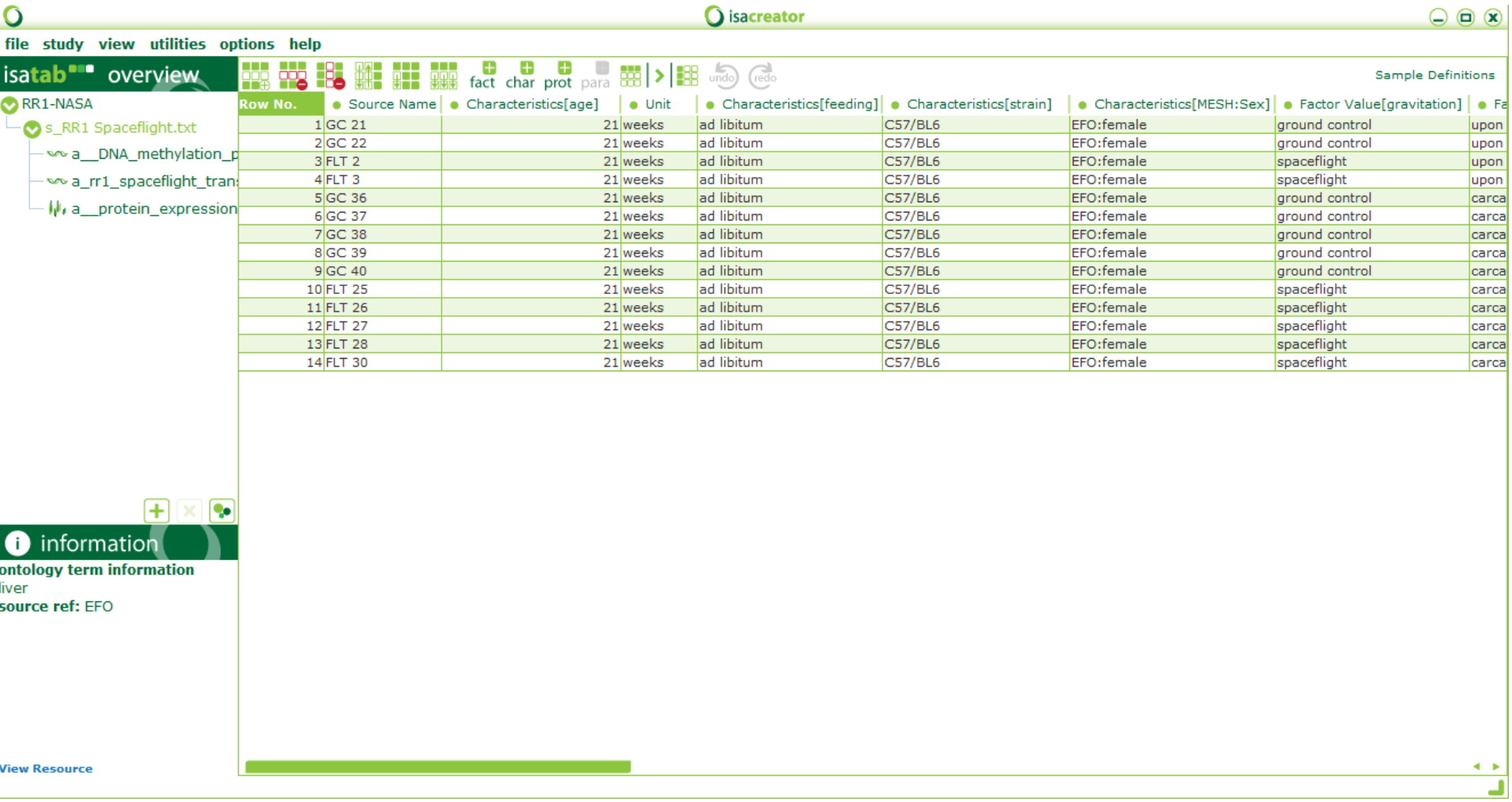
Study data hosted in the repository include a metadata definition file that is formatted according the ISA-Tab specification, which is viewable using the ISA Tools ISACreator program using a customized GeneLab configuration. Consumers of the metadata files should load this configuration, ISA configuration files, into the ISACreator program prior to loading the ISA-Tab file set, in order to view the study metadata completely and correctly.

Click the "ISA configuration files" link on GLDS repository splash page to download GeneLab customized ISACreator configuration zip package

Open GLDS ISA-Tab Files Using ISACreator Tool

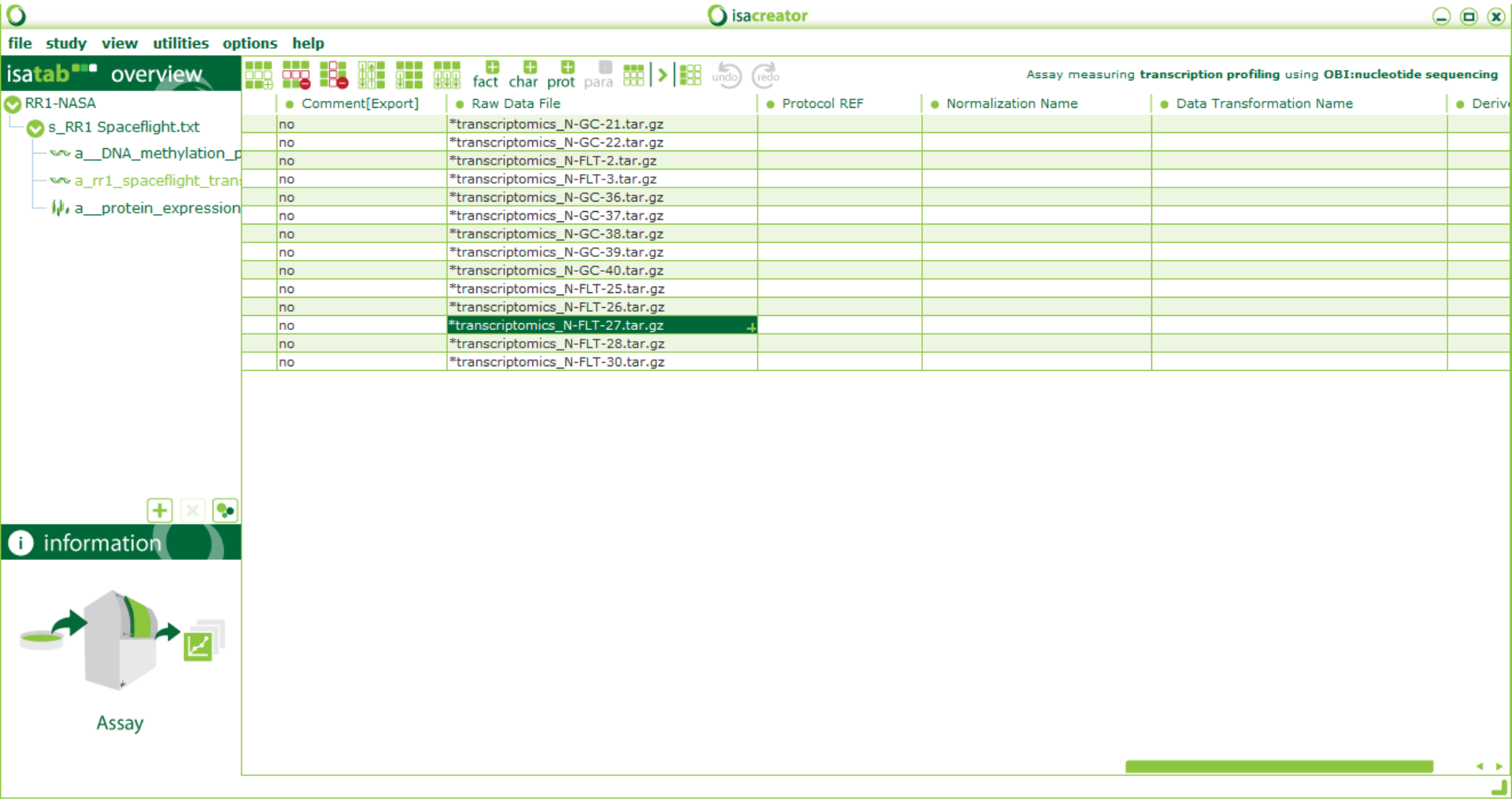


View Sample Metadata Using ISACreator Tool



Row No.	Source Name	Characteristics[age]	Unit	Characteristics[feeding]	Characteristics[strain]	Characteristics[MESH:Sex]	Factor Value[gravitation]	Fa
1	GC 21	21	weeks	ad libitum	C57/BL6	EFO:female	ground control	upon
2	GC 22	21	weeks	ad libitum	C57/BL6	EFO:female	ground control	upon
3	FLT 2	21	weeks	ad libitum	C57/BL6	EFO:female	spaceflight	upon
4	FLT 3	21	weeks	ad libitum	C57/BL6	EFO:female	spaceflight	upon
5	GC 36	21	weeks	ad libitum	C57/BL6	EFO:female	ground control	carca
6	GC 37	21	weeks	ad libitum	C57/BL6	EFO:female	ground control	carca
7	GC 38	21	weeks	ad libitum	C57/BL6	EFO:female	ground control	carca
8	GC 39	21	weeks	ad libitum	C57/BL6	EFO:female	ground control	carca
9	GC 40	21	weeks	ad libitum	C57/BL6	EFO:female	ground control	carca
10	FLT 25	21	weeks	ad libitum	C57/BL6	EFO:female	spaceflight	carca
11	FLT 26	21	weeks	ad libitum	C57/BL6	EFO:female	spaceflight	carca
12	FLT 27	21	weeks	ad libitum	C57/BL6	EFO:female	spaceflight	carca
13	FLT 28	21	weeks	ad libitum	C57/BL6	EFO:female	spaceflight	carca
14	FLT 30	21	weeks	ad libitum	C57/BL6	EFO:female	spaceflight	carca

Correlate Assay Data with Samples Using ISACreator Tool



How To Cite GeneLab

Citing NASA GeneLab Data Sets

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www.nasa.gov/directorates/heo/slpsra/

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Reference Citation:

Author (or NASA GeneLab as producer), product title, publisher (NASA GeneLab), and release date of the data product which is being credited.

Example Reference Citations:

> **For a Dataset:**
>
> Doe JQ, Smith RS. 2010. Effects of spaceflight on D. melanogaster gene expression. Dataset. Available on-line [https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-XXX/] from NASA GeneLab, NASA Ames Research Center, Moffett Field, CA.
>
> **For a Citation on a Website:**
> "D. melanogaster gene expression dataset (2015) obtained from https://genelab-data.ndc.nasa.gov/genelab/projects/, maintained by NASA GeneLab, NASA Ames Research Center, Moffett Field, CA 94035. "

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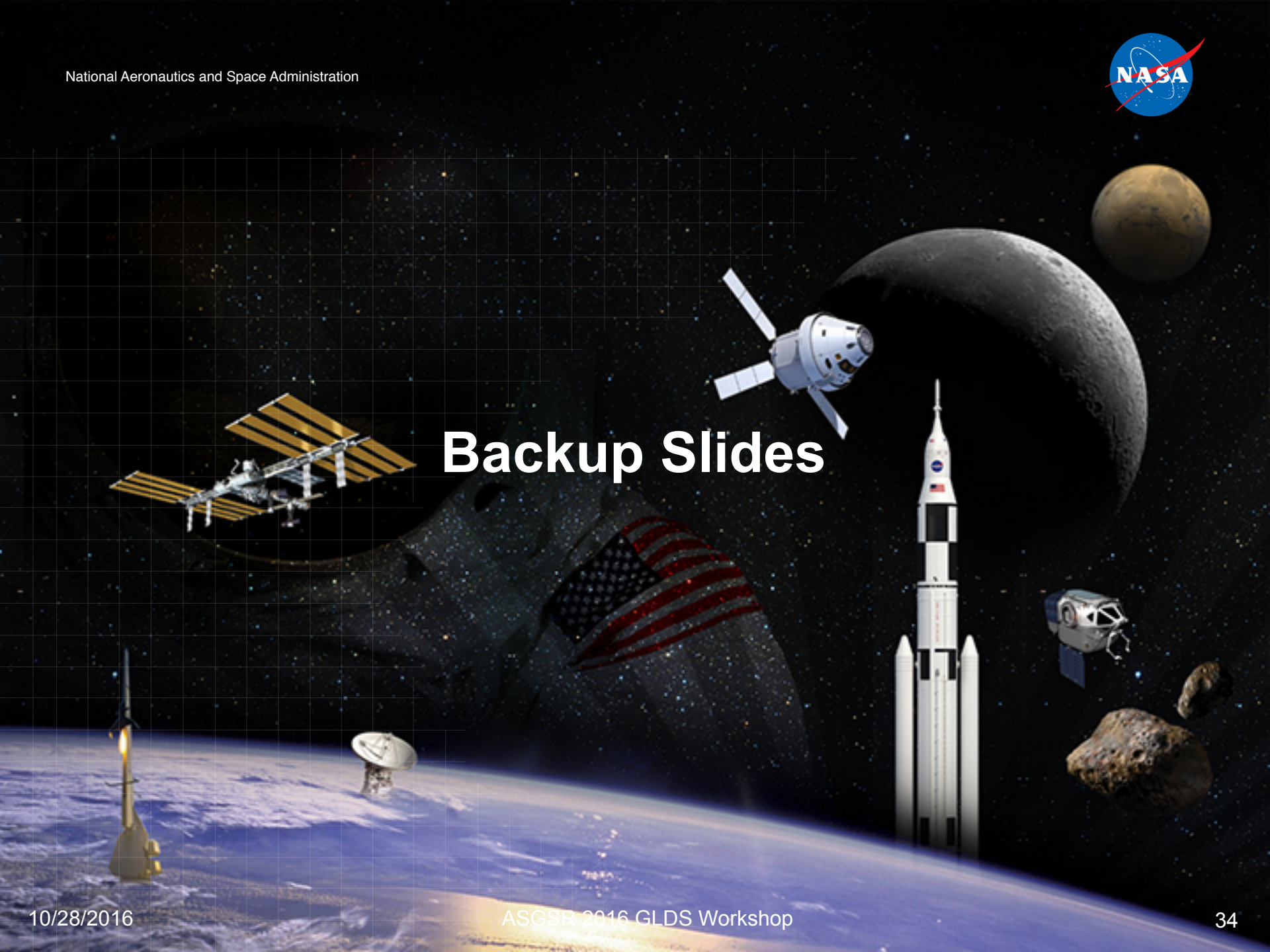
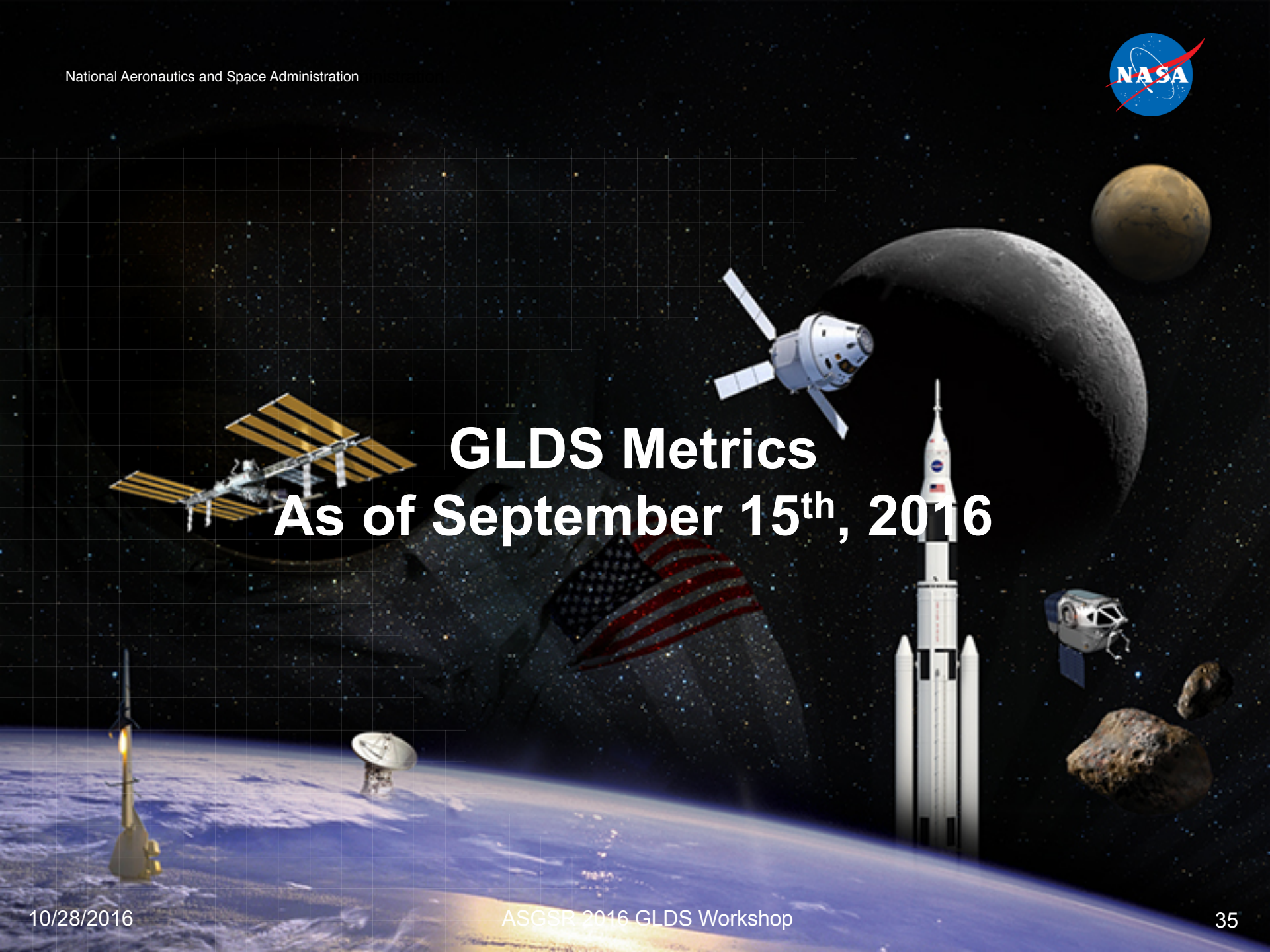
Thank You!

Contact Us

genelab-outreach@lists.nasa.gov



Backup Slides

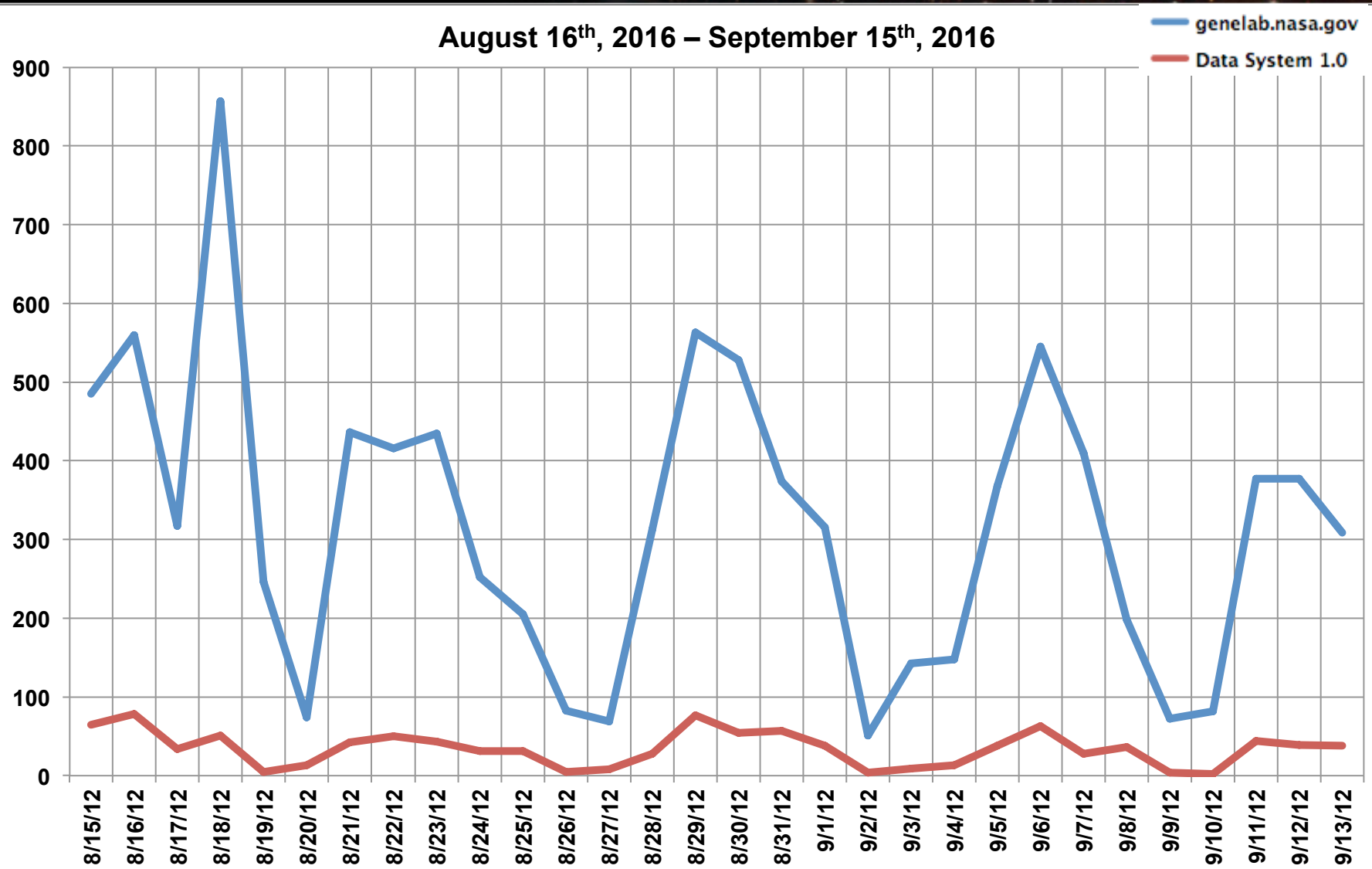


GLDS Metrics
As of September 15th, 2016

GeneLab Sites Usage

		May 16 - Jun 15	Jun 16 – Jul 15	Jul 16 – Aug 15	Aug 16 – Sep 15
Monthly Pageviews	genelab.nasa.gov	**10,505**	**11,171**	**7,130**	**9,925**
	GeneLab DS 1.0	**955**	**1,687**	**1,030**	**1,074**
Datafile Downloads - Totals					
total count		**1,048**	**1,690**	**554**	**1,103**
volume (GB)		**4,836**	**4,919**	**1,469**	**2,504**
Data File Downloads (by Species)					
Arabidopsis thaliana		399	437	35	187
Candida albicans		4	10	0	3
Drosophila melanogaster		24	56	7	22
Homo sapiens		48	102	25	110
Mus musculus		492	704	393	538
Pseudomonas aeruginosa		6	20	2	6
Rattus norvegicus		16	58	4	18
Saccharomyces cerevisiae		6	45	8	13
Salmonella enterica		4	9	0	4
Environmental Samples		9	25	0	11
Bacillus subtilis		5	12	0	4
Rhodospirillum rubrum		13	30	0	8
Caenorhabditis elegans		15	39	5	13
Escherichia coli		3	9	1	3
Ceratopteris richardii		4	10	3	2
Cellular organisms		–	55	15	81
Bacillus		–	19	14	17
Bacterial isolates		–	19	32	28
Aspergillus fumigatus		–	12	5	9
Brassica rapa		–	10	3	23
Danio rerio		–	9	2	3

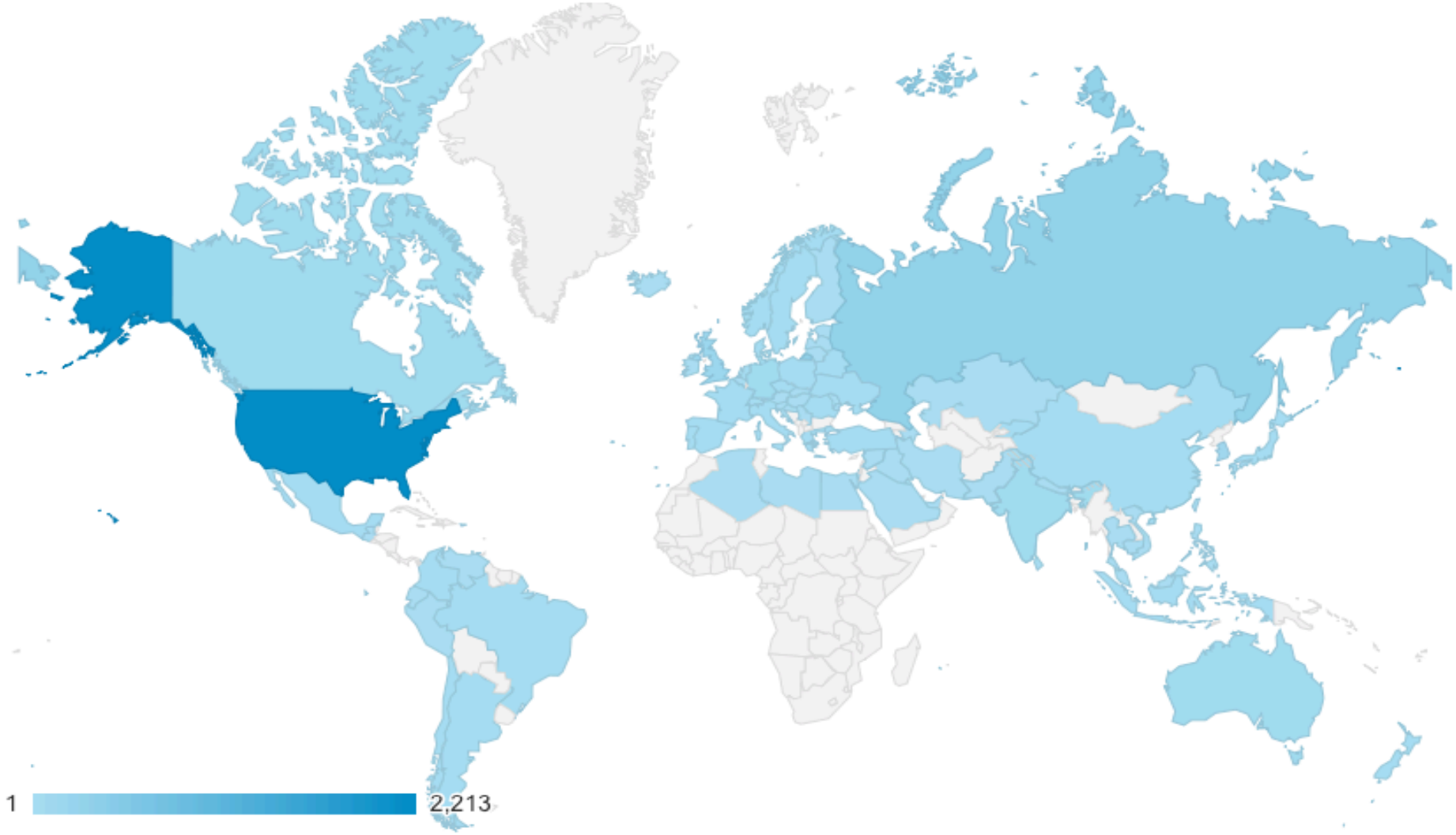
GeneLab Daily Page Views



Geographic Distribution of Users

genelab.nasa.gov (sessions/month)

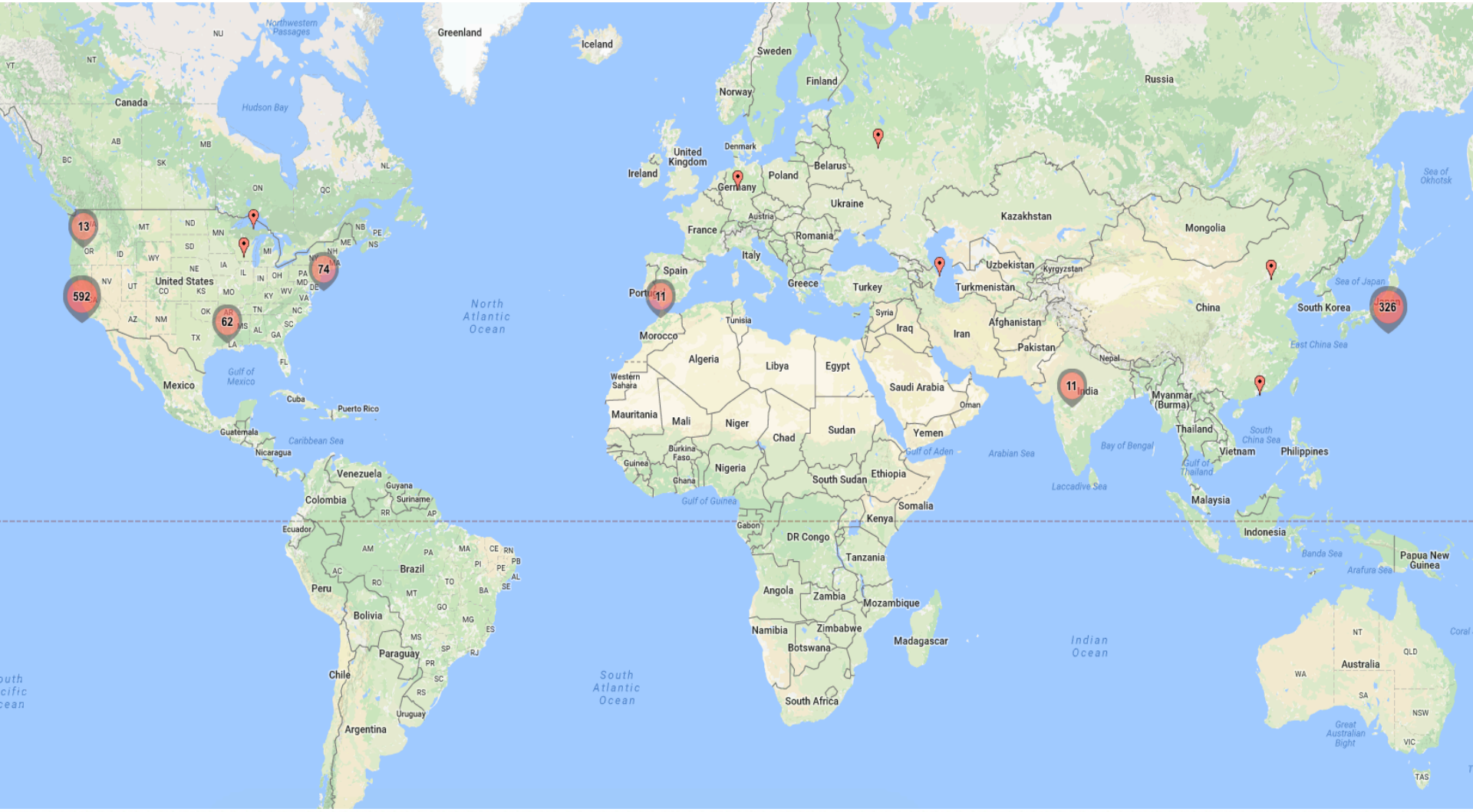
August 16th, 2016 – September 15th, 2016



GeneLab
Open Science for Exploration

Geographic Distribution of Data File Downloads

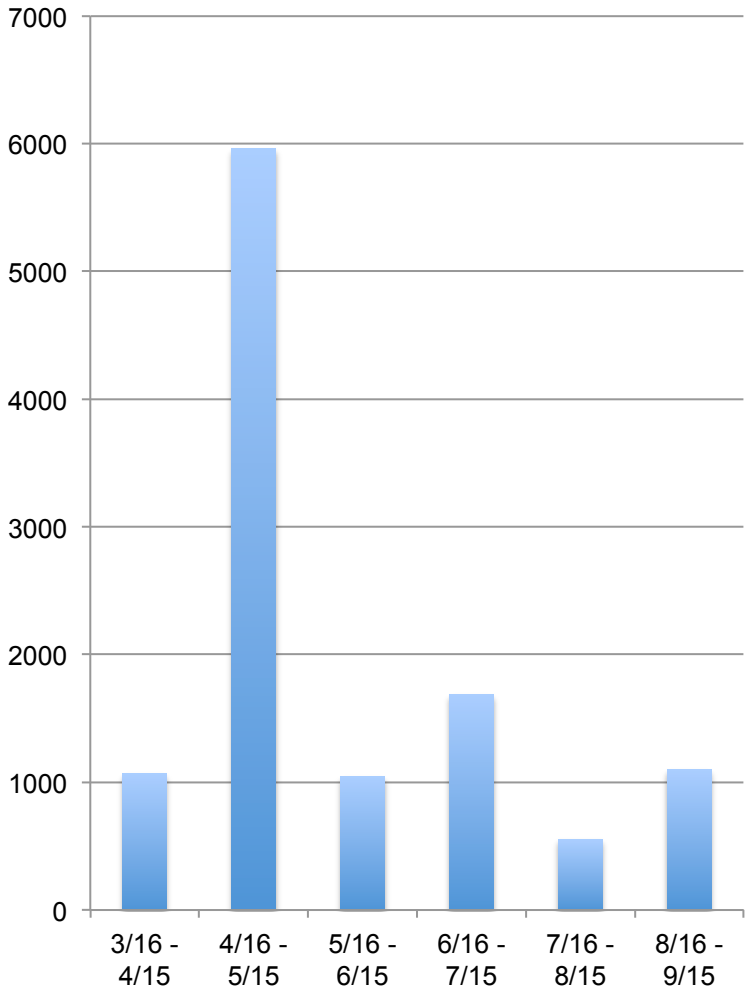
August 16th, 2016 – September 15th, 2016



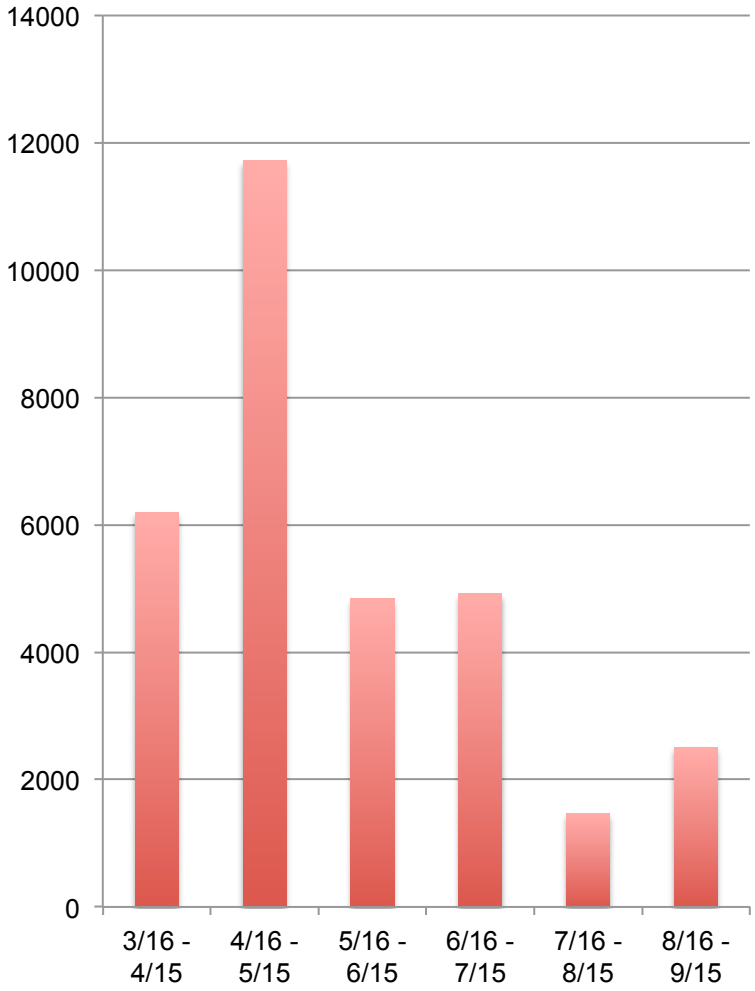
GLDS Monthly File Downloads

March 16th, 2016 - September 15th, 2016

Monthly File Downloads

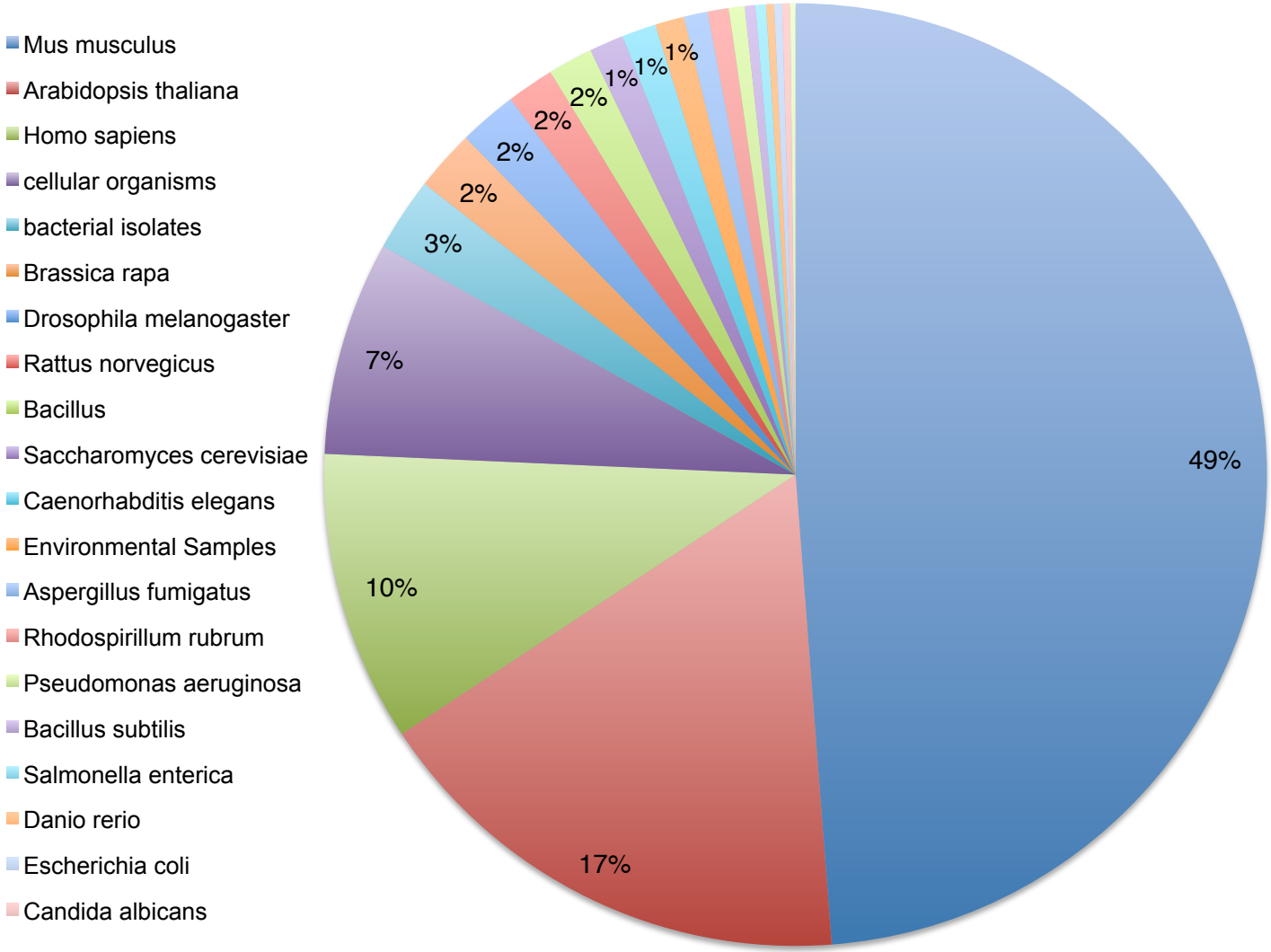


Monthly Download Volume (GB)

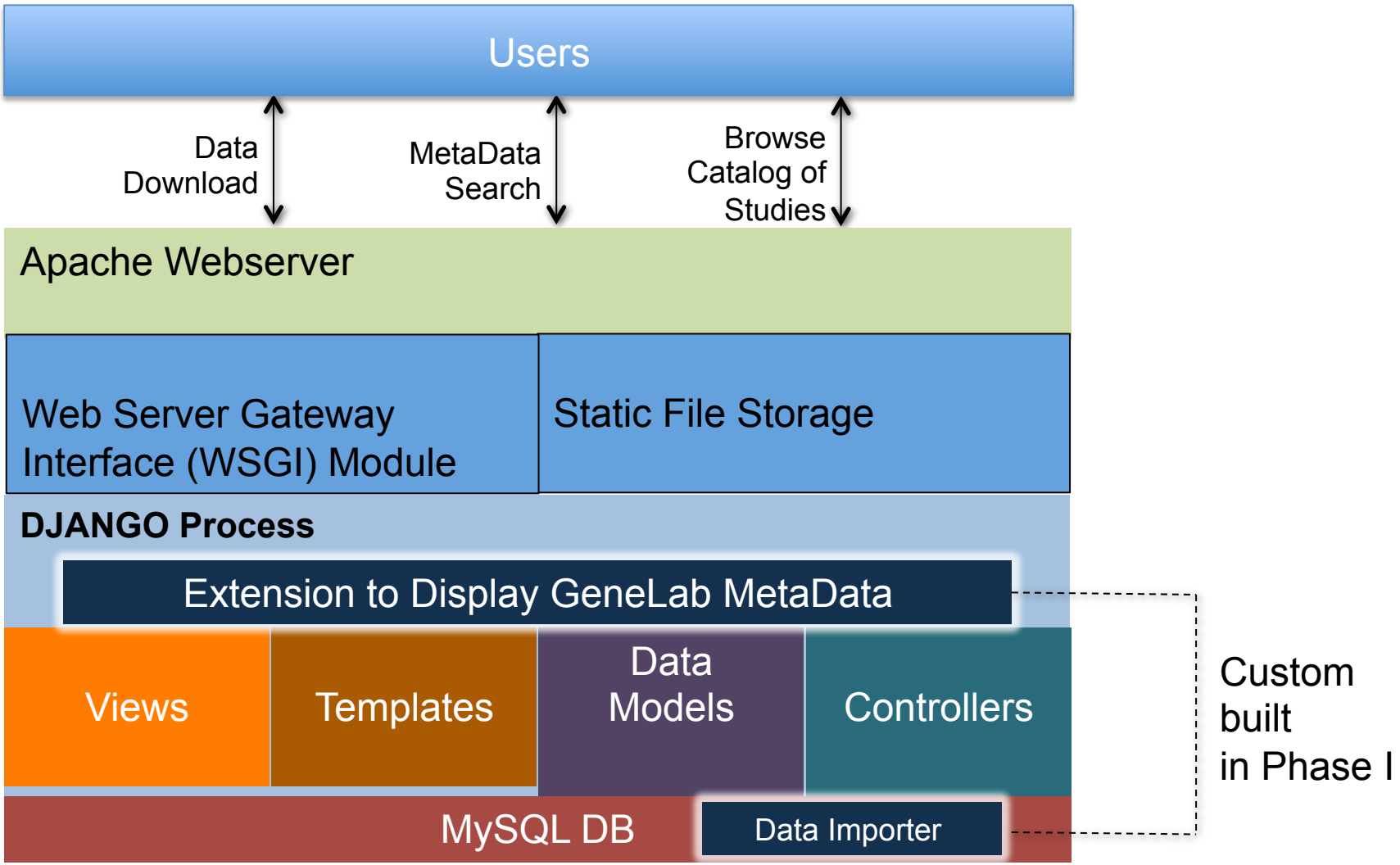


Data File Downloads by Model Organisms

August 16th, 2016 to September 15th, 2016



Phase 1 C-Gene System Architecture



GLDS Reference System Architecture